Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

1-18. **(Cancelled)**

19. **(Previously Presented)** An antibody or an antigen binding fragment thereof comprising a complementarity determining region-H3 (CDR-H3) sequence selected from the group consisting of: SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 30, and SEQ ID NO: 31.

20. **(Previously Presented)** An antibody or an antigen binding fragment thereof comprising a complementarity determining region-L3 (CDR-L3) sequence selected from the group consisting of: SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34.

21. **(Previously Presented)** An antibody or an antigen binding fragment thereof comprising a complementarity determining region-H3 (CDR-H3) sequence selected from the group consisting of: SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 30, and SEQ ID NO: 31 and a complementarity determining region-L3 (CDR-L3) sequence selected from the group consisting of: SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34.

22. **(Cancelled)**

23. **(Previously Presented)** The method of claim 40, wherein the B cells are peripheral B-cell lymphocytes or B cells from the spleen.

24. **(Previously Presented)** The method of claim 40, wherein the B cells are isolated from blood.

25. **(Previously Presented)** The method of claim 40, wherein the antigen is an immunogen.

26. **(Previously Presented)** The method of claim 40, wherein the patient displays an antibody response detectable by Western blotting in response to infection by *Clostridium difficile*.

27. **(Previously Presented)** The method of claim 40, wherein the patient has recovered from infection by *Clostridium difficile*.

28. **(Previously Presented)** The method of claim 40, wherein step (i) comprises sequencing DNA or RNA from the B cells and step (ii) comprises determining putative amino acid sequences based on the DNA or RNA sequences and wherein the set of sequences is detected among the putative amino acid sequences.

29. **(Previously Presented)** The method of claim 40, wherein step (ii) further comprises identifying CDR2 regions and detecting a set of candidate sequences among the CDR2 regions.

30. **(Previously Presented)** The method of claim 29, wherein step (ii) further comprises identifying CDR1 regions and detecting a set of candidate sequences among the CDR1 regions.

31. **(Previously Presented)** The method of claim 40, wherein step (ii) further comprises determining at least one factor from the group consisting of: the strain of *Clostridium difficile* infecting the patient; the time point at which the B cells are isolated during infection; the age of the patient; the sex of the patient; and the race of the patient; and correlating the factor with the candidate sequence.

32. **(Previously Presented)** The method of claim 40, wherein the B cells are isolated from the patient at a plurality of time points during infection.

33. **(Currently Amended)** The method of claim 40, wherein ~~the B cells are isolated from~~ step (ii) comprises detecting a plurality of sets of sequences wherein each set occurs in total at a frequency of at least one percent, and each set of sequences includes a dominant sequence and sequences of at least 80% homology to the dominant sequence and wherein steps (i) and (ii) are carried out with respect to at least two patients, ~~one~~ a first patient of whom has recovered from infection by *Clostridium difficile*, and ~~one~~ a second patient of whom has not recovered from infection by *Clostridium difficile*, wherein ~~sequences from the recovered patient are compared with sequences from the patient who has not recovered to identify sequences that are effective to clear the infection~~ step (iii) comprises comparing the sets of sequences identified in step (ii) for the first patient with the sets of sequences identified in step (ii) for the second patient and identifying a preferred set of sequences present in the first patient and absent from the second patient and confirming that an antibody or an antigen binding fragment of an antibody comprising the dominant sequence for the preferred set of sequences binds specifically to the antigen produced by *Clostridium difficile*.

34. **(Previously Presented)** The method of claim 40, wherein the B cells are isolated from at least two patients, wherein each patient has been infected by a strain of *Clostridium difficile* different from the strain that has infected the other and wherein sequences from one patient are compared with sequences from the other patient to identify a set of candidate sequences for antibodies, each of which is specific against at least one shared antigen produced by the different strains of *Clostridium difficile*.

35. **(Previously Presented)** A method of producing a database which identifies candidate sequences for antibodies specific against at least one antigen produced by *Clostridium difficile*, comprising the steps of:

(i) performing the method according to claim 40; and

(ii) storing the data produced by said method in said database.

36. **(Previously Presented)** A method of generating a report which identifies candidate sequences for antibodies specific against at least one antigen produced by *Clostridium difficile*, comprising the steps of:

(i) performing the method according to claim 40; and

(ii) producing a report comprising the data produced by said method.

37. **(Previously Presented)** A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 19.

38. **(Previously Presented)** A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 20.

39. **(Previously Presented)** A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 21.

40. **(Currently Amended)** A method for identifying candidate antigen-specific sequences of antibodies specific against at least one antigen produced by *Clostridium difficile*, the method comprising:

(i) obtaining B cells from at least one patient whose immune system has been exposed to the antigen and sequencing from the B-cells at least complementarity determining region-3 (CDR3) regions of variable heavy chains (VH) or variable light chains (VL), or both;

(ii) detecting a set of sequences that occur in total at a frequency of at least one percent, wherein the set of sequences ~~include~~ includes a dominant sequence and sequences of at least 80% homology to the dominant sequence; and

(iii) confirming that an antibody or an antigen binding fragment of an antibody comprising the dominant sequence of step (ii) binds specifically to the antigen produced by *Clostridium difficile.*

41. **(Currently Amended)** A method for identifying candidate antigen-specific sequences of antibodies specific against at least one antigen produced by *Clostridium difficile*, the method comprising:

(i) obtaining B cells from two or more patients whose immune systems have been exposed to the antigen and sequencing from the B-cells of both patients at least complementarity determining region-3 (CDR3) regions of variable heavy chains (VH) or variable light chains (VL), or both;

(ii) detecting a set of sequences that occur in the two or more patients in total at a frequency of at least one percent, wherein the set of sequences ~~include~~ includes a dominant sequence and sequences of at least 80% homology to the dominant sequence; and

(iii) confirming that an antibody or an antigen binding fragment of an antibody comprising the dominant sequence of step (ii) binds specifically to the antigen produced by *Clostridium difficile.*

42. **(Currently Amended)** A method for identifying candidate antigen-specific sequences of antibodies specific against at least one antigen produced by *Clostridium difficile*, the method comprising:

(i) obtaining B cells from at least one patient whose immune system has been exposed to the antigen and sequencing from the B-cells at least complementarity determining region-3 (CDR3) regions of variable heavy chains (VH) or variable light chains (VL), or both;

(ii) comparing the sequences of step (i) with sequences of complementarity determining region-3 (CDR3) regions of variable heavy chains (VH) or variable light chains (VL), or both, from a patient that has not been exposed to the antigen;

(iii) detecting a set of sequences that occur in total at a frequency of at least one percent in the sequences identified in step (i) and at a frequency of less than one percent in the sequences from the patient that has not been exposed to the antigen, wherein the set of sequences ~~include~~ includes a dominant sequence and sequences of at least 80% homology to the dominant sequence; and

(iv) confirming that an antibody or an antigen binding fragment of antibody comprising the dominant sequence of step (iii) binds specifically to the antigen produced by *Clostridium difficile*.

43. **(Currently Amended)** A method for identifying candidate antigen-specific sequences of antibodies specific against at least one antigen produced by *Clostridium difficile*, the method comprising:

(i) obtaining B cells from at least one patient prior to exposure of their immune system to the antigen and sequencing from the B-cells at least complementarity determining region-3 (CDR3) regions of variable heavy chains (VH) or variable light chains (VL), or both;

(ii) obtaining B cells from the patient after their immune system has been exposed to the antigen, and sequencing from the B-cells at least complementarity determining region-3 (CDR3) regions of variable heavy chains (VH) or variable light chains (VL), or both as selected in step (i);

(iii) detecting a set of sequences that occur in total at a frequency of at least one percent in the sequences identified in step (ii) and at an increased frequency with respect to the sequences identified in step (i), wherein the set of sequences ~~include~~ includes a dominant sequence and sequences of at least 80% homology to the dominant sequence; and

(iv) confirming that an antibody or an antigen binding fragment of an antibody comprising the dominant sequence of step (iii) binds specifically to the antigen produced by *Clostridium difficile*.